



0570
204

RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/992,124

Source: 01PE

Date Processed by STIC: 12/3/01

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER
VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND
TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 091992,124

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 ☐ **Wrapped Nucleics
Wrapped Aminos** The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 ☐ **Invalid Line Length** The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 ☒ **Misaligned Amino
Numbering** The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 ☐ **Non-ASCII** The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 ☐ **Variable Length** Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 ☐ **PatentIn 2.0
"bug"** A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s). Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 ☐ **Skipped Sequences
(OLD RULES)** Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 ☐ **Skipped Sequences
(NEW RULES)** Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 9 ☒ **Use of n's or Xaa's
(NEW RULES)** Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 ☐ **Invalid <213>
Response** Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 ☐ **Use of <220>** Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses.
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 ☐ **PatentIn 2.0
"bug"** Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

OIPE

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/992,124

DATE: 12/03/2001
TIME: 13:32:00

Input Set : A:\es.txt
Output Set: N:\CRF3\11212001\I992124.raw

**Does Not Comply
Corrected Diskette Needed**

Error on all pages with same mistakes repeated throughout.

Sample sequence listing attached

The type of errors shown exist throughout the Sequence Listing. Please check subsequent sequences for similar errors.

3 <110> APPLICANT: Mohammad A. Heidaran
4 Robert L. Campbell
5 Catherine A. Spargo
6 Jamie H. Wilkins
7 Perry D. Haaland

9 <120> TITLE OF INVENTION: <120. Peptides Promoting Cell Adherence, Growth and Secretion

11 <130> FILE REFERENCE: 102-410
W--> 12 <140> CURRENT APPLICATION NUMBER:
C--> 13 <141> CURRENT FILING DATE: 2001-11-19
W--> 14 <160> NUMBER OF SEQ ID: 70
15 <170> SOFTWARE:

ERRORED SEQUENCES

17 <210> SEQ ID NO: 1
18 <211> LENGTH: 5
19 <212> TYPE: PRT
C--> 20 <213> ORGANISM: Artificial Sequence
W--> 21 <220> FEATURE: Description of Artificial Sequence:
W--> 21 <220> FEATURE: Description of Artificial Sequence:
W--> 22 Synthetic peptide selected for biological activity
W--> 23 <223> OTHER INFORMATION:
E--> 23 <400> SEQUENCE: ①
24 Ile Phe Phe Lys Gly
E--> 25 ① 5

*needs only 1 and
<220> must be left blank;
explanation belongs in <223>*

27 <210> SEQ ID NO: 2
28 <211> LENGTH: 5
29 <212> TYPE: PRT
C--> 30 <213> ORGANISM: Artificial Sequence
W--> 31 <220> FEATURE: Description of Artificial Sequence:
W--> 31 <220> FEATURE: Description of Artificial Sequence:
W--> 32 Synthetic peptide selected for biological activity
W--> 33 <223> OTHER INFORMATION:
E--> 33 <400> SEQUENCE: ①
34 Phe Ile Lys Phe Gly
E--> 35 ① 5

45 <210> SEQ ID NO: 3
46 <211> LENGTH: 5
47 <212> TYPE: PRT
C--> 48 <213> ORGANISM: Artificial Sequence
W--> 49 <220> FEATURE: Description of Artificial Sequence:
W--> 49 <220> FEATURE: Description of Artificial Sequence:
W--> 50 Synthetic peptide selected for biological activity
W--> 51 <223> OTHER INFORMATION:
E--> 51 <400> SEQUENCE: ①
52 Phe Ile Phe Ala Lys

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/992,124

DATE: 12/03/2001
TIME: 13:32:00

Input Set : A:\es.txt
Output Set: N:\CRF3\11212001\I992124.raw

E--> 53 1 5
55 <210> SEQ ID NO: 4
56 <211> LENGTH: 5
57 <212> TYPE: PRT
C--> 58 <213> ORGANISM: Artificial Sequence
W--> 59 <220> FEATURE: Description of Artificial Sequence:
W--> 59 <220> FEATURE: Description of Artificial Sequence:
W--> 60 Synthetic peptide selected for biological activity
W--> 61 <223> OTHER INFORMATION:
E--> 61 <400> SEQUENCE: 0
62 Gln Val Val Ala Lys
E--> 63 1 5
65 <210> SEQ ID NO: 5
66 <211> LENGTH: 5
67 <212> TYPE: PRT
C--> 68 <213> ORGANISM: Artificial Sequence
W--> 69 <220> FEATURE: Description of Artificial Sequence:
W--> 69 <220> FEATURE: Description of Artificial Sequence:
W--> 70 Synthetic peptide selected for biological activity
W--> 71 <223> OTHER INFORMATION:
E--> 71 <400> SEQUENCE: 0
72 Phe Lys Phe Ile Gly
E--> 73 1 5
75 <210> SEQ ID NO: 6
76 <211> LENGTH: 5
77 <212> TYPE: PRT
C--> 78 <213> ORGANISM: Artificial Sequence
W--> 79 <220> FEATURE: Description of Artificial Sequence:
W--> 79 <220> FEATURE: Description of Artificial Sequence:
W--> 80 Synthetic peptide selected for biological activity
W--> 81 <223> OTHER INFORMATION:
E--> 81 <400> SEQUENCE: 0
82 Ala Phe Phe Lys Ile
E--> 83 1 5
90 <210> SEQ ID NO: 7
91 <211> LENGTH: 5
92 <212> TYPE: PRT
C--> 93 <213> ORGANISM: Artificial Sequence
W--> 94 <220> FEATURE: Description of Artificial Sequence:
W--> 94 <220> FEATURE: Description of Artificial Sequence:
W--> 95 Synthetic peptide selected for biological activity
W--> 96 <223> OTHER INFORMATION:
E--> 96 <400> SEQUENCE: 0
97 Val Phe Pro Phe Lys
E--> 98 1 5
100 <210> SEQ ID NO: 8
101 <211> LENGTH: 5
102 <212> TYPE: PRT
C--> 103 <213> ORGANISM: Artificial Sequence

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/992,124

DATE: 12/03/2001
TIME: 13:32:00

Input Set : A:\es.txt
Output Set: N:\CRF3\11212001\I992124.raw

W--> 104 <220> FEATURE: Description of Artificial Sequence:
W--> 104 <220> FEATURE: Description of Artificial Sequence:
W--> 105 Synthetic peptide selected for biological activity
W--> 106 <223> OTHER INFORMATION:
E--> 106 <400> SEQUENCE: ①
107 Ala Lys Ile Phe Phe
E--> 108 1 5
110 <210> SEQ ID NO: 9
111 <211> LENGTH: 5
112 <212> TYPE: PRT
C--> 113 <213> ORGANISM: Artificial Sequence
W--> 114 <220> FEATURE: Description of Artificial Sequence:
W--> 114 <220> FEATURE: Description of Artificial Sequence:
W--> 115 Synthetic peptide selected for biological activity
W--> 116 <223> OTHER INFORMATION:
E--> 116 <400> SEQUENCE: 0
117 Ala Phe Lys Ile Phe
E--> 118 1 5
120 <210> SEQ ID NO: 10
121 <211> LENGTH: 5
122 <212> TYPE: PRT
C--> 123 <213> ORGANISM: Artificial Sequence
W--> 124 <220> FEATURE: Description of Artificial Sequence:
W--> 124 <220> FEATURE: Description of Artificial Sequence:
W--> 125 Synthetic peptide selected for biological activity
W--> 126 <223> OTHER INFORMATION:
E--> 126 <400> SEQUENCE: 0
127 Lys Phe Ala Phe Ile
E--> 128 1 5
137 <210> SEQ ID NO: 11
138 <211> LENGTH: 5
139 <212> TYPE: PRT
C--> 140 <213> ORGANISM: Artificial Sequence
W--> 141 <220> FEATURE: Description of Artificial Sequence:
W--> 141 <220> FEATURE: Description of Artificial Sequence:
W--> 142 Synthetic peptide selected for biological activity
W--> 143 <223> OTHER INFORMATION:
E--> 143 <400> SEQUENCE: 0
144 Phe Ala Lys Phe Ile
E--> 145 1 5
147 <210> SEQ ID NO: 12
148 <211> LENGTH: 5
149 <212> TYPE: PRT
C--> 150 <213> ORGANISM: Artificial Sequence
W--> 151 <220> FEATURE: Description of Artificial Sequence:
W--> 151 <220> FEATURE: Description of Artificial Sequence:
W--> 152 Synthetic peptide selected for biological activity
W--> 153 <223> OTHER INFORMATION:
E--> 153 <400> SEQUENCE: 0

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/992,124

DATE: 12/03/2001
 TIME: 13:32:00

Input Set : A:\es.txt
 Output Set: N:\CRF3\11212001\I992124.raw

```

154 Ala Phe Phe Phe Gln
E--> 155 1 5
157 <210> SEQ ID NO: 13
158 <211> LENGTH: 5
159 <212> TYPE: PRT
C--> 160 <213> ORGANISM: Artifical Sequence
W--> 161 <220> FEATURE: Description of Artificial Sequence:
W--> 161 <220> FEATURE: Description of Artificial Sequence:
W--> 162 Synthetic peptide selected for biological activity
W--> 163 <223> OTHER INFORMATION:
E--> 163 <400> SEQUENCE: 0
E--> 164 GluGluGLuMetTyr
E--> 165 1 5
167 <210> SEQ ID NO: 14
168 <211> LENGTH: 5
169 <212> TYPE: PRT
C--> 170 <213> ORGANISM: Artifical Sequence
W--> 171 <220> FEATURE: Description of Artificial Sequence:
W--> 171 <220> FEATURE: Description of Artificial Sequence:
W--> 172 Synthetic peptide selected for biological activity
W--> 173 <223> OTHER INFORMATION:
E--> 173 <400> SEQUENCE: 0
174 Phe Ile Lys Leu Met
E--> 175 1 5
182 <210> SEQ ID NO: 15
183 <211> LENGTH: 5
184 <212> TYPE: PRT
C--> 185 <213> ORGANISM: Artifical Sequence
W--> 186 <220> FEATURE: Description of Artificial Sequence:
W--> 186 <220> FEATURE: Description of Artificial Sequence:
W--> 187 Synthetic peptide selected for biological activity
W--> 188 <223> OTHER INFORMATION:
E--> 188 <400> SEQUENCE: 0
E--> 189 Phe Phe Ile ProTyr
E--> 190 1 5
192 <210> SEQ ID NO: 16
193 <211> LENGTH: 5
194 <212> TYPE: PRT
C--> 195 <213> ORGANISM: Artifical Sequence
W--> 196 <220> FEATURE: Description of Artificial Sequence:
W--> 196 <220> FEATURE: Description of Artificial Sequence:
W--> 197 Synthetic peptide selected for biological activity
W--> 198 <223> OTHER INFORMATION:
E--> 198 <400> SEQUENCE: 0
E--> 199 PheLysLeuValTyr
E--> 200 1 5
202 <210> SEQ ID NO: 17
203 <211> LENGTH: 5
204 <212> TYPE: PRT

```

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/992,124

DATE: 12/03/2001
TIME: 13:32:00

Input Set : A:\es.txt
Output Set: N:\CRF3\11212001\I992124.raw

```
C--> 205 <213> ORGANISM: Artifical Sequence
W--> 206 <220> FEATURE: Description of Artificial Sequence:
W--> 206 <220> FEATURE: Description of Artificial Sequence:
W--> 207 Synthetic peptide selected for biological activity
W--> 208 <223> OTHER INFORMATION:
E--> 208 <400> SEQUENCE: 0
E--> 209 LysLysLysLysLys
E--> 210 1 5
      212 <210> SEQ ID NO: 18
      213 <211> LENGTH: 5
      214 <212> TYPE: PRT
C--> 215 <213> ORGANISM: Artifical Sequence
W--> 216 <220> FEATURE: Description of Artificial Sequence:
W--> 216 <220> FEATURE: Description of Artificial Sequence:
W--> 217 Synthetic peptide selected for biological activity
W--> 218 <223> OTHER INFORMATION:
E--> 218 <400> SEQUENCE: 0
E--> 219 LysLysLysLysLeu
E--> 220 1 5
      228 <210> SEQ ID NO: 19
      229 <211> LENGTH: 5
      230 <212> TYPE: PRT
C--> 231 <213> ORGANISM: Artifical Sequence
W--> 232 <220> FEATURE: Description of Artificial Sequence:
W--> 232 <220> FEATURE: Description of Artificial Sequence:
W--> 233 Synthetic peptide selected for biological activity
W--> 234 <223> OTHER INFORMATION:
E--> 234 <400> SEQUENCE: 0
E--> 235 PheLysLysLysGln
E--> 236 1 5
      238 <210> SEQ ID NO: 20
      239 <211> LENGTH: 5
      240 <212> TYPE: PRT
C--> 241 <213> ORGANISM: Artifical Sequence
W--> 242 <220> FEATURE: Description of Artificial Sequence:
W--> 242 <220> FEATURE: Description of Artificial Sequence:
W--> 243 Synthetic peptide selected for biological activity
W--> 244 <223> OTHER INFORMATION:
E--> 244 <400> SEQUENCE: 0
E--> 245 LysLysLysSerLys
E--> 246 1 5
      248 <210> SEQ ID NO: 21
      249 <211> LENGTH: 5
      250 <212> TYPE: PRT
C--> 251 <213> ORGANISM: Artifical Sequence
W--> 252 <220> FEATURE: Description of Artificial Sequence:
W--> 252 <220> FEATURE: Description of Artificial Sequence:
W--> 253 Synthetic peptide selected for biological activity
W--> 254 <223> OTHER INFORMATION:
```

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/992,124

DATE: 12/03/2001
 TIME: 13:32:00

Input Set : A:\es.txt
 Output Set: N:\CRF3\11212001\I992124.raw

```

E--> 254 <400> SEQUENCE: 0
E--> 255 LysLysLysLeuLys
E--> 256 1 5
      258 <210> SEQ ID NO: 22
      259 <211> LENGTH: 5
      260 <212> TYPE: PRT
C--> 261 <213> ORGANISM: Artificial Sequence
W--> 262 <220> FEATURE: Description of Artificial Sequence:
W--> 262 <220> FEATURE: Description of Artificial Sequence:
W--> 263 Synthetic peptide selected for biological activity
W--> 264 <223> OTHER INFORMATION:
E--> 264 <400> SEQUENCE: 0
E--> 265 PheLysLysLysLys
E--> 266 1 5
      274 <210> SEQ ID NO: 23
      275 <211> LENGTH: 5
      276 <212> TYPE: PRT
C--> 277 <213> ORGANISM: Artificial Sequence
W--> 278 <220> FEATURE: Description of Artificial Sequence:
W--> 278 <220> FEATURE: Description of Artificial Sequence:
W--> 279 Synthetic peptide selected for biological activity
W--> 280 <223> OTHER INFORMATION:
E--> 280 <400> SEQUENCE: 0
E--> 281 LeuLysLysLysLys
E--> 282 1 5
      284 <210> SEQ ID NO: 24
      285 <211> LENGTH: 5
      286 <212> TYPE: PRT
C--> 287 <213> ORGANISM: Artificial Sequence
W--> 288 <220> FEATURE: Description of Artificial Sequence:
W--> 288 <220> FEATURE: Description of Artificial Sequence:
W--> 289 Synthetic peptide selected for biological activity
W--> 290 <223> OTHER INFORMATION:
E--> 290 <400> SEQUENCE: 0
E--> 291 LysLysLeuLysLys
E--> 292 1 5
      294 <210> SEQ ID NO: 25
      295 <211> LENGTH: 5
      296 <212> TYPE: PRT
C--> 297 <213> ORGANISM: Artificial Sequence
W--> 298 <220> FEATURE: Description of Artificial Sequence:
W--> 298 <220> FEATURE: Description of Artificial Sequence:
W--> 299 Synthetic peptide selected for biological activity
W--> 300 <223> OTHER INFORMATION:
E--> 300 <400> SEQUENCE: 0
E--> 301 LysLysLysLysThr
E--> 302 1 5
      304 <210> SEQ ID NO: 26
      305 <211> LENGTH: 5

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RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/992,124

DATE: 12/03/2001
 TIME: 13:32:00

Input Set : A:\es.txt
 Output Set: N:\CRF3\11212001\I992124.raw

```

306 <212> TYPE: PRT
C--> 307 <213> ORGANISM: Artifical Sequence
W--> 308 <220> FEATURE: Description of Artificial Sequence:
W--> 308 <220> FEATURE: Description of Artificial Sequence:
W--> 309 Synthetic peptide selected for biological activity
W--> 310 <223> OTHER INFORMATION:
E--> 310 <400> SEQUENCE: 0
E--> 311 LysLysProLysLys
E--> 312 1 5
      320 <210> SEQ ID NO: 27
      321 <211> LENGTH: 5
      322 <212> TYPE: PRT
C--> 323 <213> ORGANISM: Artifical Sequence
W--> 324 <220> FEATURE: Description of Artificial Sequence:
W--> 324 <220> FEATURE: Description of Artificial Sequence:
W--> 325 Synthetic peptide selected for biological activity
W--> 326 <223> OTHER INFORMATION:
E--> 326 <400> SEQUENCE: 0
E--> 327 LysLysProGlnTyr
E--> 328 1 5
      330 <210> SEQ ID NO: 28
      331 <211> LENGTH: 5
      332 <212> TYPE: PRT
C--> 333 <213> ORGANISM: Artifical Sequence
W--> 334 <220> FEATURE: Description of Artificial Sequence:
W--> 334 <220> FEATURE: Description of Artificial Sequence:
W--> 335 Synthetic peptide selected for biological activity
W--> 336 <223> OTHER INFORMATION:
E--> 336 <400> SEQUENCE: 0
E--> 337 SerLysLysLysLys
E--> 338 1 5
      340 <210> SEQ ID NO: 29
      341 <211> LENGTH: 5
      342 <212> TYPE: PRT
C--> 343 <213> ORGANISM: Artifical Sequence
W--> 344 <220> FEATURE: Description of Artificial Sequence:
W--> 344 <220> FEATURE: Description of Artificial Sequence:
W--> 345 Synthetic peptide selected for biological activity
W--> 346 <223> OTHER INFORMATION:
E--> 346 <400> SEQUENCE: 0
E--> 347 LysVallLysLysLys
E--> 348 1 5
      350 <210> SEQ ID NO: 30
      351 <211> LENGTH: 5
      352 <212> TYPE: PRT
C--> 353 <213> ORGANISM: Artifical Sequence
W--> 354 <220> FEATURE: Description of Artificial Sequence:
W--> 354 <220> FEATURE: Description of Artificial Sequence:
W--> 355 Synthetic peptide selected for biological activity

```

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/992,124

DATE: 12/03/2001
 TIME: 13:32:00

Input Set : A:\es.txt
 Output Set: N:\CRF3\11212001\I992124.raw

```

W--> 356 <223> OTHER INFORMATION:
E--> 356 <400> SEQUENCE: 0
E--> 357 LysAsnGlnThrTyr
E--> 358 1 5
      366 <210> SEQ ID NO: 31
      367 <211> LENGTH: 5
      368 <212> TYPE: PRT
C--> 369 <213> ORGANISM: Artifical Sequence
W--> 370 <220> FEATURE: Description of Artificial Sequence:
W--> 370 <220> FEATURE: Description of Artificial Sequence:
W--> 371 Synthetic peptide selected for biological activity
W--> 372 <223> OTHER INFORMATION:
E--> 372 <400> SEQUENCE: 0
E--> 373 PheLysLysLysVal
E--> 374 1 5
      376 <210> SEQ ID NO: 32
      377 <211> LENGTH: 5
      378 <212> TYPE: PRT
C--> 379 <213> ORGANISM: Artifical Sequence
W--> 380 <220> FEATURE: Description of Artificial Sequence:
W--> 380 <220> FEATURE: Description of Artificial Sequence:
W--> 381 Synthetic peptide selected for biological activity
W--> 382 <223> OTHER INFORMATION:
E--> 382 <400> SEQUENCE: 0
E--> 383 LysProLysLysLys
E--> 384 1 5
      386 <210> SEQ ID NO: 33
      387 <211> LENGTH: 5
      388 <212> TYPE: PRT
C--> 389 <213> ORGANISM: Artifical Sequence
W--> 390 <220> FEATURE: Description of Artificial Sequence:
W--> 390 <220> FEATURE: Description of Artificial Sequence:
W--> 391 Synthetic peptide selected for biological activity
W--> 392 <223> OTHER INFORMATION:
E--> 392 <400> SEQUENCE: 0
E--> 393 PhePheLysLysLys
E--> 394 1 5
      800 <210> SEQ ID NO: 69
      801 <211> LENGTH: 5
      802 <212> TYPE: PRT
C--> 803 <213> ORGANISM: Artifical Sequence
W--> 804 <220> FEATURE: Description of Artificial Sequence:
W--> 804 <220> FEATURE: Description of Artificial Sequence:
W--> 805 Synthetic peptide selected for biological activity
W--> 806 <223> OTHER INFORMATION:
E--> 806 <400> SEQUENCE: 0
E--> 807 OrnOrnOrn
E--> 808 1 3
      810 <210> SEQ ID NO: 70
  
```

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/992,124

DATE: 12/03/2001
TIME: 13:32:00

Input Set : A:\es.txt
Output Set: N:\CRF3\11212001\I992124.raw

811 <211> LENGTH: 5
812 <212> TYPE: PRT
C--> 813 <213> ORGANISM: Artifical Sequence
W--> 814 <220> FEATURE: Description of Artificial Sequence:
W--> 814 <220> FEATURE: Description of Artificial Sequence:
W--> 815 Synthetic peptide selected for biological activity
W--> 816 <223> OTHER INFORMATION:
E--> 816 <400> SEQUENCE: 0
E--> 817 ArgArgArg
E--> 818 1 3
E--> 822 1 of 18

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/992,124

DATE: 12/03/2001

TIME: 13:32:01

Input Set : A:\es.txt

Output Set: N:\CRF3\11212001\I992124.raw

L:12 M:283 W: Missing Blank Line separator, <140> field identifier
L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:14 M:283 W: Missing Blank Line separator, <160> field identifier
L:20 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:1
L:21 M:283 W: Missing Blank Line separator, <220> field identifier
L:21 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:22 M:259 W: Allowed number of lines exceeded, <220> FEATURE:
L:23 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:23 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:1 differs:0
L:23 M:283 W: Missing Blank Line separator, <400> field identifier
L:25 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:0
L:30 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:2
L:31 M:283 W: Missing Blank Line separator, <220> field identifier
L:31 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:32 M:259 W: Allowed number of lines exceeded, <220> FEATURE:
L:33 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:33 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:2 differs:0
L:33 M:283 W: Missing Blank Line separator, <400> field identifier
L:35 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:0
L:48 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:3
L:49 M:283 W: Missing Blank Line separator, <220> field identifier
L:49 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:50 M:259 W: Allowed number of lines exceeded, <220> FEATURE:
L:51 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:51 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:3 differs:0
L:51 M:283 W: Missing Blank Line separator, <400> field identifier
L:53 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:0
L:58 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:4
L:59 M:283 W: Missing Blank Line separator, <220> field identifier
L:59 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:60 M:259 W: Allowed number of lines exceeded, <220> FEATURE:
L:61 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:61 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:4 differs:0
L:61 M:283 W: Missing Blank Line separator, <400> field identifier
L:63 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:0
L:68 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:5
L:69 M:283 W: Missing Blank Line separator, <220> field identifier
L:69 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:70 M:259 W: Allowed number of lines exceeded, <220> FEATURE:
L:71 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:71 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:5 differs:0
L:71 M:283 W: Missing Blank Line separator, <400> field identifier
L:73 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:0
L:78 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:6
L:79 M:283 W: Missing Blank Line separator, <220> field identifier
L:79 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:80 M:259 W: Allowed number of lines exceeded, <220> FEATURE:
L:81 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:

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L:81 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:6 differs:0
L:81 M:283 W: Missing Blank Line separator, <400> field identifier
L:83 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:0
L:93 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:7
L:94 M:283 W: Missing Blank Line separator, <220> field identifier
L:94 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:95 M:259 W: Allowed number of lines exceeded, <220> FEATURE:
L:96 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:96 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:7 differs:0
L:96 M:283 W: Missing Blank Line separator, <400> field identifier
L:98 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:0
L:103 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:8
L:104 M:283 W: Missing Blank Line separator, <220> field identifier
L:104 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:105 M:259 W: Allowed number of lines exceeded, <220> FEATURE:
L:106 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:106 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:8 differs:0
L:106 M:283 W: Missing Blank Line separator, <400> field identifier
L:108 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:0
L:113 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:9
L:114 M:283 W: Missing Blank Line separator, <220> field identifier
L:114 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:115 M:259 W: Allowed number of lines exceeded, <220> FEATURE:
L:116 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:116 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:9 differs:0
L:116 M:283 W: Missing Blank Line separator, <400> field identifier
L:118 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:0
L:123 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:10
L:124 M:283 W: Missing Blank Line separator, <220> field identifier
L:124 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:125 M:259 W: Allowed number of lines exceeded, <220> FEATURE:
L:126 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:126 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:10 differs:0
L:126 M:283 W: Missing Blank Line separator, <400> field identifier
L:128 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:0
L:140 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:11
L:141 M:283 W: Missing Blank Line separator, <220> field identifier
L:141 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:142 M:259 W: Allowed number of lines exceeded, <220> FEATURE:
L:143 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:143 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:11 differs:0
L:143 M:283 W: Missing Blank Line separator, <400> field identifier
L:145 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:0
L:150 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:12
L:151 M:283 W: Missing Blank Line separator, <220> field identifier
L:151 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:152 M:259 W: Allowed number of lines exceeded, <220> FEATURE:
L:153 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:153 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:12 differs:0

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L:153 M:283 W: Missing Blank Line separator, <400> field identifier
L:155 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:0
L:160 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:13
L:161 M:283 W: Missing Blank Line separator, <220> field identifier
L:161 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:162 M:259 W: Allowed number of lines exceeded, <220> FEATURE:
L:163 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:163 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:13 differs:0
L:163 M:283 W: Missing Blank Line separator, <400> field identifier
L:164 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:165 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:0
L:165 M:252 E: No. of Seq. differs, <211>LENGTH:Input:5 Found:1 SEQ:13
L:170 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:14
L:171 M:283 W: Missing Blank Line separator, <220> field identifier
L:171 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:172 M:259 W: Allowed number of lines exceeded, <220> FEATURE:
L:173 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:173 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:14 differs:0
L:173 M:283 W: Missing Blank Line separator, <400> field identifier
L:175 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:0
L:185 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:15
L:186 M:283 W: Missing Blank Line separator, <220> field identifier
L:186 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:187 M:259 W: Allowed number of lines exceeded, <220> FEATURE:
L:188 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:188 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:15 differs:0
L:188 M:283 W: Missing Blank Line separator, <400> field identifier
L:189 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:190 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:0
L:190 M:252 E: No. of Seq. differs, <211>LENGTH:Input:5 Found:4 SEQ:15
L:195 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:16
L:196 M:283 W: Missing Blank Line separator, <220> field identifier
L:196 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:197 M:259 W: Allowed number of lines exceeded, <220> FEATURE:
L:198 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:198 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:16 differs:0
L:198 M:283 W: Missing Blank Line separator, <400> field identifier
L:199 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:200 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:0
L:200 M:252 E: No. of Seq. differs, <211>LENGTH:Input:5 Found:1 SEQ:16
L:205 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:17
L:206 M:283 W: Missing Blank Line separator, <220> field identifier
L:206 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:207 M:259 W: Allowed number of lines exceeded, <220> FEATURE:
L:208 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:208 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:17 differs:0
L:208 M:283 W: Missing Blank Line separator, <400> field identifier
L:209 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:210 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:0

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L:210 M:252 E: No. of Seq. differs, <211>LENGTH:Input:5 Found:1 SEQ:17
L:215 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:18
L:216 M:283 W: Missing Blank Line separator, <220> field identifier
L:216 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:217 M:259 W: Allowed number of lines exceeded, <220> FEATURE:
L:218 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:218 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:18 differs:0
L:218 M:283 W: Missing Blank Line separator, <400> field identifier
L:219 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:220 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:0
L:220 M:252 E: No. of Seq. differs, <211>LENGTH:Input:5 Found:1 SEQ:18
L:231 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:19
L:232 M:283 W: Missing Blank Line separator, <220> field identifier
L:232 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:233 M:259 W: Allowed number of lines exceeded, <220> FEATURE:
L:234 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:234 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:19 differs:0
L:234 M:283 W: Missing Blank Line separator, <400> field identifier
L:235 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:236 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:0
L:236 M:252 E: No. of Seq. differs, <211>LENGTH:Input:5 Found:1 SEQ:19
L:241 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:20
L:242 M:283 W: Missing Blank Line separator, <220> field identifier
L:242 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:243 M:259 W: Allowed number of lines exceeded, <220> FEATURE:
L:244 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:244 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:20 differs:0
L:244 M:283 W: Missing Blank Line separator, <400> field identifier
L:245 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:246 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:0
L:246 M:252 E: No. of Seq. differs, <211>LENGTH:Input:5 Found:1 SEQ:20
L:251 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:21
L:252 M:283 W: Missing Blank Line separator, <220> field identifier
L:252 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:253 M:259 W: Allowed number of lines exceeded, <220> FEATURE:
L:254 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:254 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:21 differs:0
L:254 M:283 W: Missing Blank Line separator, <400> field identifier
L:255 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:256 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:0
L:256 M:252 E: No. of Seq. differs, <211>LENGTH:Input:5 Found:1 SEQ:21
L:261 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:22
L:262 M:283 W: Missing Blank Line separator, <220> field identifier
L:262 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:263 M:259 W: Allowed number of lines exceeded, <220> FEATURE:
L:264 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:264 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:22 differs:0
L:264 M:283 W: Missing Blank Line separator, <400> field identifier
L:265 M:333 E: Wrong sequence grouping, Amino acids not in groups!

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L:266 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:0
L:266 M:252 E: No. of Seq. differs, <211>LENGTH:Input:5 Found:1 SEQ:22
L:277 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:23
L:278 M:283 W: Missing Blank Line separator, <220> field identifier
L:278 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:279 M:259 W: Allowed number of lines exceeded, <220> FEATURE:
L:280 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:280 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:23 differs:0
L:280 M:283 W: Missing Blank Line separator, <400> field identifier
L:281 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:282 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:0
L:282 M:252 E: No. of Seq. differs, <211>LENGTH:Input:5 Found:1 SEQ:23
L:287 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:24
L:288 M:283 W: Missing Blank Line separator, <220> field identifier
L:288 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:289 M:259 W: Allowed number of lines exceeded, <220> FEATURE:
L:290 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:290 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:24 differs:0
L:290 M:283 W: Missing Blank Line separator, <400> field identifier
L:291 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:292 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:0
L:292 M:252 E: No. of Seq. differs, <211>LENGTH:Input:5 Found:1 SEQ:24
L:297 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:25
L:298 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:299 M:259 W: Allowed number of lines exceeded, <220> FEATURE:
L:300 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:300 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:25 differs:0
L:301 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:302 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:0
L:302 M:252 E: No. of Seq. differs, <211>LENGTH:Input:5 Found:1 SEQ:25
L:307 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:26
L:308 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:309 M:259 W: Allowed number of lines exceeded, <220> FEATURE:
L:310 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:310 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:26 differs:0
L:311 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:312 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:0
L:312 M:252 E: No. of Seq. differs, <211>LENGTH:Input:5 Found:1 SEQ:26
L:323 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:27
L:324 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:325 M:259 W: Allowed number of lines exceeded, <220> FEATURE:
L:326 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:326 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:27 differs:0
L:327 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:328 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:0
L:328 M:252 E: No. of Seq. differs, <211>LENGTH:Input:5 Found:1 SEQ:27
L:333 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:28
L:334 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:335 M:259 W: Allowed number of lines exceeded, <220> FEATURE:

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L:336 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:336 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:28 differs:0
L:337 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:338 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:0
L:338 M:252 E: No. of Seq. differs, <211>LENGTH:Input:5 Found:1 SEQ:28
L:343 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:29
L:344 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:345 M:259 W: Allowed number of lines exceeded, <220> FEATURE:
L:346 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:346 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:29 differs:0
L:347 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:348 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:0
L:348 M:252 E: No. of Seq. differs, <211>LENGTH:Input:5 Found:1 SEQ:29
L:353 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:30
L:354 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:355 M:259 W: Allowed number of lines exceeded, <220> FEATURE:
L:356 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:356 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:30 differs:0
L:357 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:358 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:0
L:358 M:252 E: No. of Seq. differs, <211>LENGTH:Input:5 Found:1 SEQ:30
L:369 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:31
L:370 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:371 M:259 W: Allowed number of lines exceeded, <220> FEATURE:
L:372 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:372 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:31 differs:0
L:373 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:374 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:0
L:374 M:252 E: No. of Seq. differs, <211>LENGTH:Input:5 Found:1 SEQ:31
L:379 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:32
L:380 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:381 M:259 W: Allowed number of lines exceeded, <220> FEATURE:
L:382 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:382 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:32 differs:0
L:383 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:384 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:0
L:384 M:252 E: No. of Seq. differs, <211>LENGTH:Input:5 Found:1 SEQ:32
L:389 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:33
L:390 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:391 M:259 W: Allowed number of lines exceeded, <220> FEATURE:
L:392 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:392 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:33 differs:0
L:393 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:394 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:0
L:394 M:252 E: No. of Seq. differs, <211>LENGTH:Input:5 Found:1 SEQ:33
L:399 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:34
L:400 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:401 M:259 W: Allowed number of lines exceeded, <220> FEATURE:
L:402 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:

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L:402 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:34 differs:0
L:403 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:404 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:0
L:404 M:252 E: No. of Seq. differs, <211>LENGTH:Input:5 Found:1 SEQ:34
L:415 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:35
L:416 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:417 M:259 W: Allowed number of lines exceeded, <220> FEATURE:
L:418 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:418 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:35 differs:0
L:419 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:420 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:0
L:420 M:252 E: No. of Seq. differs, <211>LENGTH:Input:5 Found:1 SEQ:35
L:425 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:36
L:426 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:427 M:259 W: Allowed number of lines exceeded, <220> FEATURE:
L:428 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:428 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:36 differs:0
L:429 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:430 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:0
L:430 M:252 E: No. of Seq. differs, <211>LENGTH:Input:5 Found:1 SEQ:36
L:435 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:37
L:436 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:437 M:259 W: Allowed number of lines exceeded, <220> FEATURE:
L:438 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:438 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:37 differs:0
L:439 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:440 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:0
L:440 M:252 E: No. of Seq. differs, <211>LENGTH:Input:5 Found:1 SEQ:37
L:445 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:38
L:446 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:447 M:259 W: Allowed number of lines exceeded, <220> FEATURE:
L:448 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:448 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:38 differs:0
L:449 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:450 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:0
L:450 M:252 E: No. of Seq. differs, <211>LENGTH:Input:5 Found:1 SEQ:38
L:461 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:39
L:462 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:463 M:259 W: Allowed number of lines exceeded, <220> FEATURE:
L:464 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:464 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:39 differs:0
L:465 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:466 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:0
L:466 M:252 E: No. of Seq. differs, <211>LENGTH:Input:5 Found:1 SEQ:39
L:471 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:40
L:472 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:473 M:259 W: Allowed number of lines exceeded, <220> FEATURE:
L:474 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:474 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:40 differs:0

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Output Set: N:\CRF3\11212001\I992124.raw

L:475 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:476 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:0
L:476 M:252 E: No. of Seq. differs, <211>LENGTH:Input:5 Found:1 SEQ:40
L:481 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:41
L:482 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:483 M:259 W: Allowed number of lines exceeded, <220> FEATURE:
L:484 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:484 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:41 differs:0
L:485 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:486 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:0
L:486 M:252 E: No. of Seq. differs, <211>LENGTH:Input:5 Found:1 SEQ:41
L:491 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:42
L:492 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:493 M:259 W: Allowed number of lines exceeded, <220> FEATURE:
L:494 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:494 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:42 differs:0
L:495 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:496 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:0
L:496 M:252 E: No. of Seq. differs, <211>LENGTH:Input:5 Found:1 SEQ:42
L:507 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:43
L:508 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:509 M:259 W: Allowed number of lines exceeded, <220> FEATURE:
L:510 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:510 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:43 differs:0
L:511 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:512 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:0
L:512 M:252 E: No. of Seq. differs, <211>LENGTH:Input:5 Found:1 SEQ:43
L:517 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:44
L:518 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:519 M:259 W: Allowed number of lines exceeded, <220> FEATURE:
L:520 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:520 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:44 differs:0
L:521 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:522 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:0
L:522 M:252 E: No. of Seq. differs, <211>LENGTH:Input:5 Found:1 SEQ:44
L:527 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:45
L:528 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:529 M:259 W: Allowed number of lines exceeded, <220> FEATURE:
L:530 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:530 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:45 differs:0
L:531 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:532 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:0
L:532 M:252 E: No. of Seq. differs, <211>LENGTH:Input:5 Found:1 SEQ:45
L:537 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:46
L:538 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:539 M:259 W: Allowed number of lines exceeded, <220> FEATURE:
L:540 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:540 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:46 differs:0
L:541 M:333 E: Wrong sequence grouping, Amino acids not in groups!

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Input Set : A:\es.txt

Output Set: N:\CRF3\11212001\I992124.raw

L:542 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:0
L:542 M:252 E: No. of Seq. differs, <211>LENGTH:Input:5 Found:1 SEQ:46
L:553 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:47
L:554 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:555 M:259 W: Allowed number of lines exceeded, <220> FEATURE:
L:556 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:556 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:47 differs:0
L:557 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:558 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:0
L:558 M:252 E: No. of Seq. differs, <211>LENGTH:Input:5 Found:1 SEQ:47
L:563 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:48
L:564 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:565 M:259 W: Allowed number of lines exceeded, <220> FEATURE:
L:566 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:566 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:48 differs:0
L:567 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:568 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:0
L:568 M:252 E: No. of Seq. differs, <211>LENGTH:Input:5 Found:1 SEQ:48
L:573 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:49
L:574 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:575 M:259 W: Allowed number of lines exceeded, <220> FEATURE:
L:576 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:576 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:49 differs:0
L:577 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:578 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:0
L:578 M:252 E: No. of Seq. differs, <211>LENGTH:Input:5 Found:1 SEQ:49
L:583 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:50
L:584 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:585 M:259 W: Allowed number of lines exceeded, <220> FEATURE:
L:586 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:586 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:50 differs:0
L:587 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:588 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:0
L:588 M:252 E: No. of Seq. differs, <211>LENGTH:Input:5 Found:1 SEQ:50
L:603 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:604 M:252 E: No. of Seq. differs, <211>LENGTH:Input:5 Found:1 SEQ:51
L:613 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:614 M:252 E: No. of Seq. differs, <211>LENGTH:Input:5 Found:1 SEQ:52
L:623 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:624 M:252 E: No. of Seq. differs, <211>LENGTH:Input:5 Found:1 SEQ:53
L:633 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:634 M:252 E: No. of Seq. differs, <211>LENGTH:Input:55 Found:1 SEQ:54
L:649 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:650 M:252 E: No. of Seq. differs, <211>LENGTH:Input:5 Found:1 SEQ:55
L:659 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:660 M:252 E: No. of Seq. differs, <211>LENGTH:Input:5 Found:1 SEQ:56
L:669 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:670 M:252 E: No. of Seq. differs, <211>LENGTH:Input:5 Found:1 SEQ:57
L:679 M:333 E: Wrong sequence grouping, Amino acids not in groups!

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Input Set : A:\es.txt

Output Set: N:\CRF3\11212001\I992124.raw

L:680 M:252 E: No. of Seq. differs, <211>LENGTH:Input:5 Found:1 SEQ:58
L:695 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:696 M:252 E: No. of Seq. differs, <211>LENGTH:Input:5 Found:1 SEQ:59
L:705 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:706 M:252 E: No. of Seq. differs, <211>LENGTH:Input:5 Found:1 SEQ:60
L:715 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:716 M:252 E: No. of Seq. differs, <211>LENGTH:Input:5 Found:1 SEQ:61
L:725 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:726 M:252 E: No. of Seq. differs, <211>LENGTH:Input:5 Found:1 SEQ:62
L:741 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:742 M:252 E: No. of Seq. differs, <211>LENGTH:Input:5 Found:1 SEQ:63
L:807 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1

<400>	1						
agctgtagtc	atccctgtgt	cctcttctct	ctgggcctct	cacctctgcta	atcagatctc		60
agggagagtg	tcttgacctt	cctctgcctt	tgcagcttca	caggcaggca	ggcaggcagc		120
tgatgtggca	atctgtggca	gtgccacagg	ctttctagcc	aggcttaggg	tgggtctccgc		180
cgcggcgcgg	cggccctctt	cgcgcctctc	tcgcgcctct	ctctctgctct	cctctctgctc		240

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ggacctgatt	aggtgagcag	gaggagggggg	cggttagc	atg	gtt	tca	atg	ttc	agc	296						
				Met	Val	Ser	Met	Phe	Ser							
				1				5								
ttg	tct	ttc	aaa	tgg	cct	gga	ttt	tgt	ttg	ttt	gtt	tgt	ttg	ttc	caa	344
Leu	Ser	Phe	Lys	Trp	Pro	Gly	Phe	Cys	Leu	Phe	Val	Cys	Leu	Phe	Gln	
			10					15					20			
tgt	ccc	aaa	gtc	ctc	ccc	tgt	cac	tca	tca	ctg	cag	ccg	aat	ctt		389
Cys	Pro	Lys	Val	Leu	Pro	Cys	His	Ser	Ser	Leu	Gln	Pro	Asn	Leu		
		25					30					35				

<210> 2
<211> 37
<212> PRT
<213> Paramecium sp.

<400>	2															
Met	Val	Ser	Met	Phe	Ser	Leu	Ser	Phe	Lys	Trp	Pro	Gly	Phe	Cys	Leu	
1				5					10					15		
Phe	Val	Cys	Leu	Phe	Gln	Cys	Pro	Lys	Val	Leu	Pro	Cys	His	Ser	Ser	
			20					25					30			

Leu Gln Pro Asn Leu
35

<210> 3
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Designed peptide based on size and polarity to act as a linker between the alpha and beta chains of Protein XYZ.

<400>	3										
Met	Val	Asn	Leu	Glu	Pro	Met	His	Thr	Glu	Ile	
1				5					10		

<210> 4
<400> 4
000

[Annex VIII follows]

identifiers and their accompanying information as shown in the following table. The numeric identifier shall be used only in the "Sequence Listing." The order and presentation of the items of information in the "Sequence Listing" shall conform to the arrangement given below. Each item of information shall begin on a new line and shall begin with the numeric identifier enclosed in angle brackets as shown. The submission of those items of information designated with an "M" is mandatory. The submission of those items of information designated with an "O" is optional. Numeric identifiers <110> through <170> shall only be set forth at the beginning of the "Sequence Listing." The following table illustrates the numeric identifiers.

Numeric Identifier	Definition	Comments and Format	Mandatory (M) or Optional (O)
<110>	Applicant	Preferably max. of 10 names; one name per line; preferable format: Surname, Other Names and/or Initials	M
<120>	Title of Invention		M
<130>	File Reference	Personal file reference	M, when filed prior to assignment of appl. number
<140>	Current Application Number	Specify as: US 07/999,999 or PCT/US96/99999	M, if available
<141>	Current Filing Date	Specify as: yyyy-mm-dd	M, if available
<150>	Prior Application Number	Specify as: US 07/999,999 or PCT/US96/99999	M, if applicable include priority documents under 35 USC 119 and 120
<151>	Prior Application Filing Date	Specify as: yyyy-mm-dd	M, if applicable
<160>	Number of SEQ ID NOs	Count includes total number of SEQ ID NOs	M
<170>	Software	Name of software used to create the Sequence Listing	O
<210>	SEQ ID NO: #:	Response shall be an integer representing the SEQ ID NO shown	M
<211>	Length	Respond with an integer expressing the number of bases or amino acid residues	M

<212>	Type	Whether presented sequence molecule is DNA, RNA, or PRT (protein). If a nucleotide sequence contains both DNA and RNA fragments, the type shall be "DNA." In addition, the combined DNA/RNA molecule shall be further described in the <220> to <223> feature section.	M
<213>	Organism	Scientific name, i.e. Genus/species, Unknown or Artificial Sequence. In addition, the "Unknown" or "Artificial Sequence" organisms shall be further described in the <220> to <223> feature section.	M
<220>	Feature	Leave blank after <220>. <221-223> provide for a description of points of biological significance in the sequence.	M, under the following conditions: if "n," "Xaa," or a modified or unusual L-amino acid or modified base was used in a sequence; if ORGANISM is "Artificial Sequence" or "Unknown"; if molecule is combined DNA/RNA.
<221>	Name/Key	Provide appropriate identifier for feature, preferably from WIPO Standard ST.25 (1998), Appendix 2, Tables 5 and 6	M, under the following conditions: if "n," "Xaa," or a modified or unusual L-amino acid or modified base was used in a sequence
<222>	Location	Specify location within sequence; where appropriate state number of first and last bases/amino acids	M, under the following conditions: if "n," "Xaa," or a modified or unusual L-amino acid or modified

		in feature	base was used in a sequence
<223>	Other Information	Other relevant information; four lines maximum	M, under the following conditions: if "n," "Xaa," or a modified or unusual L-amino acid or modified base was used in a sequence; if ORGANISM is "Artificial Sequence" or "Unknown"; if molecule is combined DNA/RNA.
<300>	Publication Information	Leave blank after <300>	0
<301>	Authors	Preferably max of ten named authors of publication; specify one name per line; preferable format: Surname, Other Names and/or Initials	0
<302>	Title		0
<303>	Journal		0
<304>	Volume		0
<305>	Issue		0
<306>	Pages		0
<307>	Date	Journal date on which data published; specify as yyyy-mm-dd, MMM-yyyy or Season-yyyy	0
<308>	Database Accession Number	Accession number assigned by database including database name	0
<309>	Database Entry Date	Date of entry in database; specify as yyyy-mm-dd or MMM-yyyy	0
<310>	Patent Document Number	Document number; for patent-type citations only. Specify as, for example, US 07/999,999	0

<311>	Patent Filing Date	Document filing date, for patent-type citations only; specify as yyyy-mm-dd	0
<312>	Publication Date	Document publication date, for patent-type citations only; specify as yyyy-mm-dd	0
<313>	Relevant Residues	FROM (position) TO (position)	0
<400>	Sequence	SEQ ID NO should follow the numeric identifier and should appear on the line preceding the actual sequence	0

5. Section 1.024 is revised to read as follows:

1.024 Form and format for nucleotide and/or amino acid sequence submissions in computer readable form.

(a) The computer readable form required by 1.021(c) shall meet the following specifications:

(1) The computer readable form shall contain a single "Sequence Listing" as either a diskette, series of diskettes, or other permissible media outlined in paragraph (c) of this section.

(2) The "Sequence Listing" in paragraph (a) (1) of this section shall be submitted in American Standard Code for Information Interchange (ASCII) text. No other formats shall be allowed.

(3) The computer readable form may be created by any means, such as word processors, nucleotide/amino acid sequence editors or other custom computer programs; however, it shall conform to all specifications detailed in this section.

(4) File compression is acceptable when using diskette media, so long as the compressed file is in a self-extracting format that will decompress on one of the systems described in paragraph (b) of this section.

(5) Page numbering shall not appear within the computer readable form version of the "Sequence Listing" file.

(6) All computer readable forms shall have a label permanently affixed thereto on which has been hand-printed or typed: the name of the applicant, the title of the invention, the date on which the data were recorded on the computer readable form, the operating system used, a reference number, and an application serial number and filing date, if known.

(b) Computer readable form submissions must meet these format requirements:

(1) Computer: IBM PC/XT/AT, or compatibles, or Apple Macintosh;

(2) Operating System: MS-DOS, Unix or Macintosh;